SEQUENCE LISTING

<110> Corena T. McMANUS
David A. JONES

<120> METHYL-CPG BINDING DOMAIN PROTEIN 2 HOMOLOGS

<130> 38509-0016US1

<140>
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<150> PCT/US03/10631
<151> 2003-04-07

<150> 60/369,851
<151> 2002-04-05

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<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
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ctttacagaa gaaacgagaa atccacatgg ccaaggccca tcggagacga gctgcgaggt 180
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Lys Leu Lys Arg Asn Met Met Pro Trp Ala Leu Gln Lys Lys Arg Glu
20 25 30

Ile His Met Ala Lys Ala His Arg Arg Arg Ala Ala Arg Ser Ala Leu

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         35                  40                  45

Pro Met Arg Leu Thr Ser Cys Ile Phe Arg Arg Pro Val Thr Arg Ile
     50                  55                  60

Arg Ser His Pro Asp Asn Gln Val Arg Arg Arg Lys Gly Asp Glu His
 65                  70                  75                  80

Leu Glu Lys Pro Gln Gln Leu Cys Ala Tyr Arg Arg Leu Gln Ala Leu
                85                  90                  95

Gln Pro Cys Ser Ser Gln Gly Glu Gly Ser Ser Pro Leu His Leu Glu
            100                 105                 110

Ser Val Leu Ser Ile Leu Ala Pro Gly Thr Ala Ser Glu Ser Leu Asp
        115                 120                 125

Arg Ala Gly Ala Glu Arg Val Arg Ser Pro Leu Glu Pro Thr Pro Gly
    130                 135                 140

Arg Phe Pro Ala Val Ala Gly Gly Pro Thr Pro Gly Met Gly Cys Gln
145                 150                 155                 160

Leu Pro Pro Pro Leu Ser Gly Gln Leu Val Thr Pro Ala Asp Ile Arg
                165                 170                 175

Arg Gln Ala Arg Arg Val Lys Lys Ala Arg Glu Arg Leu Ala Lys Ala
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Leu Gln Ala Asp Arg Leu Ala Arg Gln Ala Glu Met Leu Thr Cys Arg
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agttcacaga ggaagcaacg tgactgtgta aaccaatgca aatcaaagcc tggcttgagc 180
acctcaatcc ctttgagaat gtccagttac acattcaaga ggccagtaac gagaattaca 240
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20 25 30

Tyr Thr Phe Lys Arg Pro Val Thr Arg Ile Thr Pro His Pro Gly Asn
35 40 45

Glu Val Arg Tyr His Gln Trp Glu Glu Ser Leu Glu Lys Pro Gln Gln
50 55 60

Val Cys Trp Gln Arg Arg Leu Gln Gly Leu Gln Ala Tyr Ser Ser Ala
65 70 75 80

Gly Glu Leu Ser Ser Thr Leu Asp Leu Ala Asn Thr Leu Gln Lys Leu
85 90 95

Val Pro Ser Tyr Thr Gly Gly Ser Leu Leu Glu Asp Leu Ala Ser Gly
100 105 110

Leu Glu His Ser Cys Pro Met Pro His Leu Ala Cys Ser Ser Asp Ala
115 120 125

Val Glu Ile Ile Pro Ala Glu Gly Val Gly Ile Ser Gln Leu Leu Cys
130 135 140

Lys Gln Phe Leu Val Thr Glu Glu Asp Ile Arg Lys Gln Glu Gly Lys
145 150 155 160

Val Lys Thr Val Arg Glu Arg Leu Ala Ile Ala Leu Ile Ala Asp Gly
165 170 175

Leu Ala Asn Glu Ala Glu Lys Val Arg Asp Gln Glu Gly Cys Pro Glu
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Lys Arg

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20 25 30

Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln Leu Ala Arg Tyr Leu
35 40 45

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Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe Arg Thr Gly Lys Met
     50                  55                  60

Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn Asp Pro
 65                  70                  75                  80

Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu Pro Ile
                85                  90                  95

Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val Thr Asn
            100                 105                 110

His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn Glu Gln
        115                 120                 125

Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser Ala Ser
    130                 135                 140

Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys Gly Leu
145                 150                 155                 160

Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser Ala Val
                165                 170                 175

Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln Val Ser
            180                 185                 190

Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser Gln Pro
        195                 200                 205

Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys Gln Glu
    210                 215                 220

Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu Met Ala
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Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile Glu Met
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<212> PRT
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             20                  25                  30

Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
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          35                  40                  45

Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
     50                  55                  60

Arg Thr Gly Lys Met Leu Met Ser Lys Met Asn Lys Ser Arg Gln Arg
 65                  70                  75                  80

Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
                 85                  90                  95

Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
            100                 105                 110

Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
        115                 120                 125

Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
    130                 135                 140

Gly Leu Asn Ala Phe Asp Ile Ala Glu Glu Leu Val Lys Thr Met Asp
145                 150                 155                 160

Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
                165                 170                 175

Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Met Pro Ile
            180                 185                 190

Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
        195                 200                 205

Asn Thr Thr Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Glu Asp
    210                 215                 220

Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
225                 230                 235                 240

Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
                245                 250                 255

Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Asp Asp Asp Glu
            260                 265                 270

Glu Asp Glu Glu Glu Glu Glu Glu Glu Pro Asp Pro Asp Pro Glu Met
        275                 280                 285

Glu His Val
    290
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